SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Bahija Jallal
                                      Gregory D. Plowman

    (ii) TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
                                        PTP04 RELATED DISORDERS

    (iii) NUMBER OF SEQUENCES: 18

    (iv) CORRESPONDENCE ADDRESS:

        (A) ADDRESSEE: Lyon & Lyon
        (B) STREET: 633 West Fifth Street
                            Suite 4700
        (C) CITY: Los Angeles
        (D) STATE: California
        (E) COUNTRY: U.S.A.
        (F) ZIP: 90071-2066

    (v) COMPUTER READABLE FORM:

        (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                            storage
        (B) COMPUTER: IBM Compatible
        (C) OPERATING SYSTEM: IBM P.C. DOS 5.0
        (D) SOFTWARE: FastSEQ for Windows 2.0

    (vi) CURRENT APPLICATION DATA:

        (A) APPLICATION NUMBER: To Be Assigned
        (B) FILING DATE: Herewith
        (C) CLASSIFICATION:

    (vii) PRIOR APPLICATION DATA:

        (A) APPLICATION NUMBER: 60/047,222
        (B) FILING DATE: May 20, 1997

    (viii) ATTORNEY/AGENT INFORMATION:

        (A) NAME: Warburg, Richard J.
        (B) REGISTRATION NUMBER: 32,327
        (C) REFERENCE/DOCKET NUMBER: 234/253

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(2)   INFORMATION FOR SEQ ID NO: 1:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 3580 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
CCCGGGTGCC CTCCCTCAAC CTACTTATAG ACTATTTTTC TTGCTCTGCA GCATGGACCA    60
AAGAGAAATT CTGCAGAAGT TCCTGGATGA GGCCCAAAGC AAGAAAATTA CTAAAGAGGA   120
GTTTGCCAAT GAATTCTGA AGCTGAAAAG GCAATCTACC AAGTACAAGG CAGACAAAAC   180
CTATCCTACA ACTGTGGCTG AGAAGCCCAA GAATATCAAG AAAAACAGAT ATAAGGATAT   240
TTTGCCCTAT GATTATAGCC GGGTAGAACT ATCCCTGATA ACCTCTGATG AGGATTCCAG   300
CTACATCAAT GCCAACTTCA TTAAGGGAGT TTATGGACCC AAGGCTTATA TTGCCACCCA   360
GGGTCCTTTA TCTACAACCC TCCTGGACTT CTGGAGGATG ATTTGGGAAT ATAGTGTCCT   420
TATCATTGTT ATGGCATGCA TGGAGTATGA AATGGGAAAG AAAAAGTGTG AGCGCTACTG   480
GGCTGAGCCA GGAGAGATGC AGCTGGAATT TGGCCCTTTC TCTGTATCCT GTGAAGCTGA   540
AAAAAGGAAA TCTGATTATA TAATCAGGAC TCTAAAAGTT AAGTTCAATA GTGAAACTCG   600
AACTATCTAC CAGTTTCATT ACAAGAATTG GCCAGACCAT GATGTACCTT CATCTATAGA   660
CCCTATTCTT GAGCTCATCT GGGATGTACG TTGTTACCAA GAGGATGACA GTGTTCCCAT   720
ATGCATTCAC TGCAGTGCTG GCTGTGGAAG GACTGGTGTT ATTTGTGCTA TTGATTATAC   780
ATGGATGTTG CTAAAAGATG GGATAATTCC TGAGAACTTC AGTGTTTTCA GTTTGATCCG   840
GGAAATGCGG ACACAGAGGC CTTCATTAGT TCAAACGCAG GAACAATATG AACTGGTCTA   900
CAATGCTGTA TTAGAACTAT TTAAGAGACA GATGGATGTT ATCAGAGATA AACATTCTGG   960
AACAGAGAGT CAAGCAAAGC ATTGTATTCC TGAGAAAAAT CACACTCTCC AAGCAGACTC  1020
TTATTCTCCT AATTTACCAA AAAGTACCAC AAAAGCAGCA AAAATGATGA ACCAACAAAG  1080
GACAAAAATG GAAATCAAAG AATCTTCTTC CTTTGACTTT AGGACTTCTG AAATAAGTGC  1140
AAAAGAAGAG CTAGTTTTGC ACCCTGCTAA ATCAAGCACT TCTTTTGACT TTCTGGAGCT  1200
AAATTACAGT TTTGACAAAA ATGCTGACAC AACCATGAAA TGGCAGACAA AGGCATTTCC  1260
AATAGTTGGG GAGCCTCTTC AGAAGCATCA AGTTTGGAT TTGGGCTCTC TTTTGTTTGA  1320
GGGATGTTCT AATTCTAAAC CTGTAAATGC AGCAGGAAGA TATTTTAATT CAAAGGTGCC  1380
AATAACACGG ACCAAATCAA CTCCTTTTGA ATTGATACAG CAGAGAGAAA CCAAGGAGGT  1440
GGACAGCAAG GAAAACTTTT CTTATTTGGA ATCTCAACCA CATGATTCTT GTTTTGTAGA  1500
GATGCAGGCT CAAAAAGTAA TGCATGTTTC TTCAGCAGAA CTGAATTATT CACTGCCATA  1560
TGACTCTAAA CACCAAATAC GTAATGCCTC TAATGTAAAG CACCATGACT CTAGTGCTCT  1620
TGGTGTATAT TCTTACATAC CTTTAGTGGA AAATCCTTAT TTTTCATCAT GGCCTCCAAG  1680
TGGTACCAGT TCTAAGATGT CTCTTGATTT ACCTGAGAAG CAAGATGGAA CTGTTTTTCC  1740
TTCTTCTCTG TTGCCAACAT CCTCTACATC CCTCTTCTCT TATTACAATT CACATGATTC  1800
TTTATCACTG AATTCTCCAA CCAATATTTC CTCACTATTG AACCAGGAGT CAGCTGTACT  1860
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AGCAACTGCT CCAAGGATAG ATGATGAAAT CCCCCCTCCA CTTCCTGTAC GGACACCTGA    1920
ATCATTTATT GTGGTTGAGG AAGCTGGAGA ATTCTCACCA AATGTTCCCA AATCCTTATC    1980
CTCAGCTGTG AAGGTAAAAA TTGGAACATC ACTGGAATGG GGTGGAACAT CTGAACCAAA    2040
GAAATTTGAT GACTCTGTGA TACTTAGACC AAGCAAGAGT GTAAAACTCC GAAGTCCTAA    2100
ATCAGAACTA CATCAAGATC GTTCTTCTCC CCCACCTCCT CTCCCAGAAA GAACTCTAGA    2160
GTCCTTCTTT CTTGCCGATG AAGATTGTAT GCAGGCCCAA TCTATAGAAA CATATTCTAC    2220
TAGCTATCCT GACACCATGG AAAATTCAAC ATCTTCAAAA CAGACACTGA AGACTCCTGG    2280
AAAAAGTTTC ACAAGGAGTA AGAGTTTGAA AATTTTGCGA AACATGAAAA AGAGTATCTG    2340
TAATTCTTGC CCACCAAACA AGCCTGCAGA ATCTGTTCAG TCAAATAACT CCAGCTCATT    2400
TCTGAATTTT GGTTTTGCAA ACCGTTTTTC AAAACCCAAA GGACCAAGGA ATCCACCACC    2460
AACTTGGAAT ATTTAATAAA ACTCCAGATT TATAATAATA TGGGCTGCAA GTACACCTGC    2520
AAATAAAACT ACTAGAATAC TGCTAGTTAA AATAAGTGCT CTATATGCAT AATATCAAAT    2580
ATGAAGATAT GCTAATGTGT TAATAGCTTT TAAAAGAAAA GCAAAATGCC AATAAGTGCC    2640
AGTTTTGCAT TTTCATATCA TTTGCATTGA GTTGAAAACT GCAAATAAAA GTTTGTCACT    2700
TGAGCTTATG TACAGAATGC TATATGAGAA ACACTTTTAG AATGGATTTA TTTTTCATTT    2760
TTGCCAGTTA TTTTTATTTT CTTTTACTTT TTTACATAAA CATAAACTTC AAAAGGTTTG    2820
TAAGATTTGG ATCTCAACTA ATTTCTACAT TGCCAGAATA TACTATAAAA AGTTAAAAAA    2880
AAACTTACTT TGTGGGTTGC AATACAAACT GCTCTTGACA ATGACTATTC CCTGACAGTT    2940
ATTTTTGCCT AAATGGAGTA TACCTTGTAA ATCTTCCCAA ATGTTGTGGA AAACTGGAAT    3000
ATTAAGAAAA TGAGAAATTA TATTTATTAG AATAAAATGT GCAAATAATG ACAATTATTT    3060
GAATGTAACA AGGAATTCAA CTGAAATCCT GATAAGTTTT AACCAAAGTC ATTAAATTAC    3120
CAATTCTAGA AAAGTAATCA ATGAAATATA ATAGCTATCT TTTGGTAGCA AAAGATATAA    3180
ATTGTATATG TTTATACAGG ATCTTTCAGA TCATGTGCAA TTTTTATCTA ACCAATCAGA    3240
AATACTAGTT TAAAATGAAT TTCTATATGA ATATGGATCT GCCATAAGAA AATCTAGTTC    3300
AACTCTAATT TTATGTAGTA AATAAATTGG CAGGTAATTG TTTTTACAAA GAATCCACCT    3360
GACTTCCCCT AATGCATTAA AAATATTTTT ATTTAAATAA CTTTATTTAT AACTTTTAGA    3420
AACATGTAGT ATTGTTTAAA CATCATTTGT TCTTCAGTAT TTTTCATTTG GAAGTCCAAT    3480
AGGGCAAATT GAATGAAGTA TTATTATCTG TCTCTTGTAG TACAATGTAT CCAACAGACA    3540
CTCAATAAAC TTTTTGGTTG TTAAAAAAAA AAAAAAAAA                           3580
```

   (2)   INFORMATION FOR SEQ ID NO: 2:

        (i) SEQUENCE CHARACTERISTICS:

             (A)   LENGTH: 807 amino acids
             (B)   TYPE: amino acid
             (C)   STRANDEDNESS: single
             (D)   TOPOLOGY: linear

       (ii) MOLECULE TYPE: peptide

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Asp Gln Arg Glu Ile Leu Gln Lys Phe Leu Asp Glu Ala Gln Ser
1               5                   10                  15

Lys Lys Ile Thr Lys Glu Glu Phe Ala Asn Glu Phe Leu Lys Leu Lys
            20              25                  30
```

Arg Gln Ser Thr Lys Tyr Lys Ala Asp Lys Thr Tyr Pro Thr Thr Val
        35   40   45

Ala Glu Lys Pro Lys Asn Ile Lys Lys Asn Arg Tyr Lys Asp Ile Leu
        50   55   60

Pro Tyr Asp Tyr Ser Arg Val Glu Leu Ser Leu Ile Thr Ser Asp Glu
65   70   75   80

Asp Ser Ser Tyr Ile Asn Ala Asn Phe Ile Lys Gly Val Tyr Gly Pro
                85   90   95

Lys Ala Tyr Ile Ala Thr Gln Gly Pro Leu Ser Thr Thr Leu Leu Asp
                100   105   110

Phe Trp Arg Met Ile Trp Glu Tyr Ser Val Leu Ile Ile Val Met Ala
        115   120   125

Cys Met Glu Tyr Glu Met Gly Lys Lys Lys Cys Glu Arg Tyr Trp Ala
        130   135   140

Glu Pro Gly Glu Met Gln Leu Glu Phe Gly Pro Phe Ser Val Ser Cys
145   150   155   160

Glu Ala Glu Lys Arg Lys Ser Asp Tyr Ile Ile Arg Thr Leu Lys Val
                165   170   175

Lys Phe Asn Ser Glu Thr Arg Thr Ile Tyr Gln Phe His Tyr Lys Asn
                180   185   190

Trp Pro Asp His Asp Val Pro Ser Ser Ile Asp Pro Ile Leu Glu Leu
        195   200   205

Ile Trp Asp Val Arg Cys Tyr Gln Glu Asp Asp Ser Val Pro Ile Cys
        210   215   220

Ile His Cys Ser Ala Gly Cys Gly Arg Thr Gly Val Ile Cys Ala Ile
225   230   235   240

Asp Tyr Thr Trp Met Leu Leu Lys Asp Gly Ile Ile Pro Glu Asn Phe
                245   250   255

Ser Val Phe Ser Leu Ile Arg Glu Met Arg Thr Gln Arg Pro Ser Leu
                260   265   270

Val Gln Thr Gln Glu Gln Tyr Glu Leu Val Tyr Asn Ala Val Leu Glu
        275   280   285

Leu Phe Lys Arg Gln Met Asp Val Ile Arg Asp Lys His Ser Gly Thr
        290   295   300

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Glu Ser Gln Ala Lys His Cys Ile Pro Glu Lys Asn His Thr Leu Gln
305   310   315   320

Ala Asp Ser Tyr Ser Pro Asn Leu Pro Lys Ser Thr Thr Lys Ala Ala
            325   330   335

Lys Met Met Asn Gln Gln Arg Thr Lys Met Glu Ile Lys Glu Ser Ser
            340   345   350

Ser Phe Asp Phe Arg Thr Ser Glu Ile Ser Ala Lys Glu Glu Leu Val
            355   360   365

Leu His Pro Ala Lys Ser Ser Thr Ser Phe Asp Phe Leu Glu Leu Asn
        370   375   380

Tyr Ser Phe Asp Lys Asn Ala Asp Thr Thr Met Lys Trp Gln Thr Lys
385   390   395   400

Ala Phe Pro Ile Val Gly Glu Pro Leu Gln Lys His Gln Ser Leu Asp
            405   410   415

Leu Gly Ser Leu Leu Phe Glu Gly Cys Ser Asn Ser Lys Pro Val Asn
        420   425   430

Ala Ala Gly Arg Tyr Phe Asn Ser Lys Val Pro Ile Thr Arg Thr Lys
        435   440   445

Ser Thr Pro Phe Glu Leu Ile Gln Gln Arg Glu Thr Lys Glu Val Asp
    450   455   460

Ser Lys Glu Asn Phe Ser Tyr Leu Glu Ser Gln Pro His Asp Ser Cys
465   470   475   480

Phe Val Glu Met Gln Ala Gln Lys Val Met His Val Ser Ser Ala Glu
            485   490   495

Leu Asn Tyr Ser Leu Pro Tyr Asp Ser Lys His Gln Ile Arg Asn Ala
        500   505   510

Ser Asn Val Lys His His Asp Ser Ser Ala Leu Gly Val Tyr Ser Tyr
        515   520   525

Ile Pro Leu Val Glu Asn Pro Tyr Phe Ser Ser Trp Pro Pro Ser Gly
        530   535   540

Thr Ser Ser Lys Met Ser Leu Asp Leu Pro Glu Lys Gln Asp Gly Thr
545   550   555   560

Val Phe Pro Ser Ser Leu Leu Pro Thr Ser Ser Thr Ser Leu Phe Ser
            565   570   575

Tyr Tyr Asn Ser His Asp Ser Leu Ser Leu Asn Ser Pro Thr Asn Ile
                580   585   590

Ser Ser Leu Leu Asn Gln Glu Ser Ala Val Leu Ala Thr Ala Pro Arg
                595   600   605

Ile Asp Asp Glu Ile Pro Pro Pro Leu Pro Val Arg Thr Pro Glu Ser
                610   615   620

Phe Ile Val Val Glu Glu Ala Gly Glu Phe Ser Pro Asn Val Pro Lys
625   630   635   640

Ser Leu Ser Ser Ala Val Lys Val Lys Ile Gly Thr Ser Leu Glu Trp
                645   650   655

Gly Gly Thr Ser Glu Pro Lys Lys Phe Asp Asp Ser Val Ile Leu Arg
                660   665   670

Pro Ser Lys Ser Val Lys Leu Arg Ser Pro Lys Ser Glu Leu His Gln
                675   680   685

Asp Arg Ser Ser Pro Pro Pro Pro Leu Pro Glu Arg Thr Leu Glu Ser
                690   695   700

Phe Phe Leu Ala Asp Glu Asp Cys Met Gln Ala Gln Ser Ile Glu Thr
705   710   715   720

Tyr Ser Thr Ser Tyr Pro Asp Thr Met Glu Asn Ser Thr Ser Ser Lys
                725   730   735

Gln Thr Leu Lys Thr Pro Gly Lys Ser Phe Thr Arg Ser Lys Ser Leu
                740   745   750

Lys Ile Leu Arg Asn Met Lys Lys Ser Ile Cys Asn Ser Cys Pro Pro
                755   760   765

Asn Lys Pro Ala Glu Ser Val Gln Ser Asn Asn Ser Ser Ser Phe Leu
                770   775   780

Asn Phe Gly Phe Ala Asn Arg Phe Ser Lys Pro Lys Gly Pro Arg Asn
785   790   795   800

Pro Pro Pro Thr Trp Asn Ile
                805

(2) INFORMATION FOR SEQ ID NO: 3:

    (i) SEQUENCE CHARACTERISTICS:

         (A) LENGTH: 23 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

    (ix) FEATURE:

         (D) OTHER INFORMATION: The letter "Y" stands for C or T.
                                  The letter "V" stands for A, C or
                                     G.
                                  The letter "R" stands for A or G.
                                  The letter "N" stands for A, C, G
                                     or T.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

                                                               23
GAYTTYTGGV RNATGRTNTG GGA

(2) INFORMATION FOR SEQ ID NO: 4:

    (i) SEQUENCE CHARACTERISTICS:

         (A) LENGTH: 23 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
         (D) TOPOLOGY: linear

    (ix) FEATURE:

         (D) OTHER INFORMATION: The letter "S" stands for C or G.
                                  The letter "Y" stands for C or T.
                                  The letter "N" stands for A, C, G
                                     or T.
                                  The letter "W" stands for A or T.
                                  The letter "R" stands for A or G.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

                                                               23
CGGCCSAYNC CNGCNSWRCA RTG

(2) INFORMATION FOR SEQ ID NO: 5:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 8 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:

        (D) OTHER INFORMATION: "Xaa" in positions 4 and 6 stand
                                  for an unspecified amino acid.
                                  "Xaa" in position 8 stands for
                                  either Glu or Asp.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Asp Phe Trp Xaa Met Xaa Trp Xaa
 1   5

(2) INFORMATION FOR SEQ ID NO: 6:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 7 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (ix) FEATURE:

        (D) OTHER INFORMATION: "Xaa" in positions 3 and 6 stand
                                  for an unspecified amino acid.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

His Cys Xaa Ala Gly Xaa Gly
 1   5

(2)   INFORMATION FOR SEQ ID NO: 7:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 34 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CACCGTTCGA GTATTTCAGA TTGTGAAGAA GTCC   34

(2)   INFORMATION FOR SEQ ID NO: 8:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 34 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGACTTCTTC ACAATCTGAA ATACTCGAAC GGTG   34

(2)   INFORMATION FOR SEQ ID NO: 9:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 33 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCGTTATGTG AGGAAGAGCC ACATTACAGG ACC   33

(2)   INFORMATION FOR SEQ ID NO: 10:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 33 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GGTCCTGTAA TGTGGCTCTT CCTCACATAA CGG   33

(2)   INFORMATION FOR SEQ ID NO: 11:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 23 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 11:

                                                             23
GGCATGCATG GAGTATGAAA TGG

(2)   INFORMATION FOR SEQ ID NO: 12:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 30 base pairs
        (B)   TYPE: nucleic acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 12:

                                                             30
CGTACATCCC AGATGAGCTC AAGAATAGGG

(2)   INFORMATION FOR SEQ ID NO: 13:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 10 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ii)   MOLECULE TYPE: peptide

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 1   5   10

(2)   INFORMATION FOR SEQ ID NO: 14:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 5 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ii)   MOLECULE TYPE: peptide

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 14:

His Cys Ser Ala Gly
 1   5

(2)   INFORMATION FOR SEQ ID NO: 15:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 31 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ii)   MOLECULE TYPE: peptide

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Ser Trp Pro Pro Ser Gly Thr Ser Ser Lys Met Ser Leu Asp Asp Leu
 1   5   10   15

Pro Glu Lys Gln Asp Gly Thr Val Phe Pro Ser Ser Leu Leu Pro
       20   25   30

(2)   INFORMATION FOR SEQ ID NO: 16:

    (i)   SEQUENCE CHARACTERISTICS:

        (A)   LENGTH: 30 amino acids
        (B)   TYPE: amino acid
        (C)   STRANDEDNESS: single
        (D)   TOPOLOGY: linear

    (ii)   MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: .16:

Tyr Ser Leu Pro Tyr Asp Ser Lys His Gln Ile Arg Asn Ala Ser Asn
1   5   10   15

Val Lys His His Asp Ser Ser Ala Leu Gly Val Tyr Ser Tyr
            20   25   30

(2) INFORMATION FOR SEQ ID NO: 17:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 30 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

His Thr Leu Gln Ala Asp Ser Tyr Ser Pro Asn Leu Pro Lys Ser Thr
1   5   10   15

Thr Lys Ala Ala Lys Met Met Asn Gln Gln Arg Thr Lys Cys
            20   25   30

(2) INFORMATION FOR SEQ ID NO: 18:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 802 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: peptide

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Asp Gln Arg Glu Ile Leu Gln Gln Leu Leu Lys Glu Ala Gln Lys
1   5   10   15

Lys Lys Leu Asn Ser Glu Glu Phe Ala Ser Glu Phe Leu Lys Leu Lys
            20   25   30

Arg Gln Ser Thr Lys Tyr Lys Ala Asp Lys Ile Tyr Pro Thr Thr Val
        35   40   45

Ala Gln Arg Pro Lys Asn Ile Lys Lys Asn Arg Tyr Lys Asp Ile Leu
        50   55   60

Pro Tyr Asp His Ser Leu Val Glu Leu Ser Leu Leu Thr Ser Asp Glu
65   70   75   80

Asp Ser Ser Tyr Ile Asn Ala Ser Phe Ile Lys Gly Val Tyr Gly Pro
                85   90   95

Lys Ala Tyr Ile Ala Thr Gln Gly Pro Leu Ser Thr Thr Leu Leu Asp
                100   105   110

Phe Trp Arg Met Ile Trp Glu Tyr Arg Ile Leu Val Ile Val Met Ala
                115   120   125

Cys Met Glu Phe Glu Met Gly Lys Lys Lys Cys Glu Arg Tyr Trp Ala
            130   135   140

Glu Pro Gly Glu Thr Gln Leu Gln Phe Gly Pro Phe Ser Ile Ser Cys
145   150   155   160

Glu Ala Glu Lys Lys Lys Ser Asp Tyr Lys Ile Arg Thr Leu Lys Ala
                165   170   175

Lys Phe Asn Asn Glu Thr Arg Ile Ile Tyr Gln Phe His Tyr Lys Asn
                180   185   190

Trp Pro Asp His Asp Val Pro Ser Ser Ile Asp Pro Ile Leu Gln Leu
            195   200   205

Ile Trp Asp Met Arg Cys Tyr Gln Glu Asp Asp Cys Val Pro Ile Cys
        210   215   220

Ile His Cys Ser Ala Gly Cys Gly Arg Thr Gly Val Ile Cys Ala Val
225   230   235   240

Asp Tyr Thr Trp Met Leu Leu Lys Asp Gly Ile Ile Pro Lys Asn Phe
                245   250   255

Ser Val Phe Asn Leu Ile Gln Glu Met Arg Thr Gln Arg Pro Ser Leu
            260   265   270

Val Gln Thr Gln Glu Gln Tyr Glu Leu Val Tyr Ser Ala Val Leu Glu
        275   280   285

Leu Phe Lys Arg His Met Asp Val Ile Ser Asp Asn His Leu Gly Arg
        290   295   300

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Glu Ile Gln Ala Gln Cys Ser Ile Pro Glu Gln Ser Leu Thr Val Glu
305   310   315   320

Ala Asp Ser Cys Pro Leu Asp Leu Pro Lys Asn Ala Met Arg Asp Val
            325   330   335

Lys Thr Thr Asn Gln His Ser Lys Gln Gly Ala Glu Ala Glu Ser Thr
            340   345   350

Gly Gly Ser Ser Leu Gly Leu Arg Thr Ser Thr Met Asn Ala Glu Glu
            355   360   365

Glu Leu Val Leu His Ser Ala Lys Ser Ser Pro Ser Phe Asn Cys Leu
            370   375   380

Glu Leu Asn Cys Gly Cys Asn Asn Lys Ala Val Ile Thr Arg Asn Gly
385   390   395   400

Gln Ala Arg Ala Ser Pro Val Val Gly Glu Pro Leu Gln Lys Tyr Gln
                405   410   415

Ser Leu Asp Phe Gly Ser Met Leu Phe Gly Ser Cys Pro Ser Ala Leu
            420   425   430

Pro Ile Asn Thr Ala Asp Arg Tyr His Asn Ser Lys Gly Pro Val Lys
            435   440   445

Arg Thr Lys Ser Thr Pro Phe Glu Leu Ile Gln Gln Arg Lys Thr Asn
            450   455   460

Asp Leu Ala Val Gly Asp Gly Phe Ser Cys Leu Glu Ser Gln Leu His
465   470   475   480

Glu His Tyr Ser Leu Arg Glu Leu Gln Val Gln Arg Val Ala His Val
            485   490   495

Ser Ser Glu Glu Leu Asn Tyr Ser Leu Pro Gly Ala Cys Asp Ala Ser
            500   505   510

Cys Val Pro Arg His Ser Pro Gly Ala Leu Arg Val His Leu Tyr Thr
            515   520   525

Ser Leu Ala Glu Asp Pro Tyr Phe Ser Ser Ser Pro Pro Asn Ser Ala
            530   535   540

Asp Ser Lys Met Ser Phe Asp Leu Pro Glu Lys Gln Asp Gly Ala Thr
545   550   555   560

Ser Pro Gly Ala Leu Leu Pro Ala Ser Ser Thr Thr Ser Phe Phe Tyr
            565   570   575

Ser Asn Pro His Asp Ser Leu Val Met Asn Thr Leu Thr Ser Phe Ser
            580   585   590

Pro Pro Leu Asn Gln Glu Thr Ala Val Glu Ala Pro Ser Arg Arg Thr
        595   600   605

Asp Asp Glu Ile Pro Pro Pro Leu Pro Glu Arg Thr Pro Glu Ser Phe
    610   615   620

Ile Val Val Glu Glu Ala Gly Glu Pro Ser Pro Arg Val Thr Glu Ser
625   630   635   640

Leu Pro Leu Val Val Thr Phe Gly Ala Ser Pro Glu Cys Ser Gly Thr
                645   650   655

Ser Glu Met Lys Ser His Asp Ser Val Gly Phe Thr Pro Ser Lys Asn
            660   665   670

Val Lys Leu Arg Ser Pro Lys Ser Asp Arg His Gln Asp Gly Ser Pro
        675   680   685

Pro Pro Pro Leu Pro Glu Arg Thr Leu Glu Ser Phe Phe Leu Ala Asp
    690   695   700

Glu Asp Cys Ile Gln Ala Gln Ala Val Gln Thr Ser Ser Thr Ser Tyr
705   710   715   720

Pro Glu Thr Thr Glu Asn Ser Thr Ser Ser Lys Gln Thr Leu Arg Thr
                725   730   735

Pro Gly Lys Ser Phe Thr Arg Ser Lys Ser Leu Lys Ile Phe Arg Asn
            740   745   750

Met Lys Lys Ser Val Cys Asn Ser Ser Ser Pro Ser Lys Pro Thr Glu
        755   760   765

Arg Val Gln Pro Lys Asn Ser Ser Ser Phe Leu Asn Phe Gly Phe Gly
    770   775   780

Asn Arg Phe Ser Lys Pro Lys Gly Pro Arg Asn Pro Pro Ser Ala Trp
785   790   795   800

Asn Met

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